



#9

## SEQUENCE LISTING

&lt;110&gt; Barber, Elizabeth K

&lt;120&gt; Gene Expression Control Element DNA

&lt;130&gt; 896034605001

&lt;140&gt; US 09/966,264

&lt;141&gt; 2001-09-28

&lt;150&gt; US 60/237,079

&lt;151&gt; 2000-09-30

&lt;160&gt; 61

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&lt;211&gt; 137

&lt;212&gt; DNA

&lt;213&gt; human

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Thr Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys  
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Val Ile Asn Gln Ser Leu Ile Ala Lys Val Glu Lys Met Tyr Pro  
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Ile Met Glu Tyr Ser Cys Ser Asp Arg Asn Leu Val Leu Ile Tyr Gly  
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Leu	Cys	Cys	Leu	His	Pro	Glu	Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys
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Glu	Thr	Glu		Cys	Tyr	Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe
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ctt	tct	ctt	tgt	ttt	cca	gga	cac	aat	gta	gga	agt	ctt	ttc	cac	atg 480
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Gln	Val	Cys	Thr	Ile	Ile	Arg	Asn	Thr	Pro	Lys	Pro	Lys		Gly	Arg		
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Ile Tyr Ile Tyr Ile Gly Asn Leu Asn Met Lys Lys Glu Gln Asn Lys	35	40	45
Cys Phe Thr Thr Pro Asp Ser Arg Met Val Phe Ile Ile Phe Ile Gln	50	55	60
Gln Arg Gly Leu Asp Ser Lys Ser Leu Gln Glu Ile Asn Leu Tyr Phe	65	70	75
Cys Glu Gly Phe Tyr Thr Ser Met Gln Leu Tyr Lys Lys Val Ile Arg	85	90	95
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Lys	Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	
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Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu	Met	
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Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr	Leu	Ser	
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Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe	Pro	Gly	His	
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Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu	Gly	Arg	Ala	Met	
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Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu	Gly	Ala	Glu	Lys	Met	
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Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	
		180						185					190			
Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu	
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Arg	Arg	Val	Val	Val	Leu	Tyr	Cys	Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	
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Gln	Lys	Ser	Tyr	Lys	Lys	Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	
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Leu	Ala	Ile	Ser	Leu	Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	
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Lys	Gln	Leu	Lys	Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	
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Gly Gln Val Val Lys Leu Arg Thr Gln Val Cys Thr Ile Ile Arg Asn  
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 Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala Thr Ser  
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acc ata gcc tca gaa gca agc caa cag cct gaa aca gct ttg aaa tga 144  
 Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala Leu Lys  
 35 40 45

aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc gat ggt 192  
 Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp Gly  
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Glu Glu Gly Ala Glu  
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aaa tga aaa gtt ggt gtg gcg gtg atg gtg gca gtg ata atg gtg acc -48  
 Lys Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr  
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	Val	Ile	Asn	Gln	Ser	Leu	Ile	Ala	Lys	Val	Glu	Lys	Met	Tyr	Pro	
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Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val	Leu	Ile	Tyr	Gly	
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Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu	Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	
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Asp	Glu	Glu	Gly	Ala	Glu		Met	Phe	Tyr	Asn	Ser		Phe	Pro	His	
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ggg	ttt	tat	aat	att	cat	aca	aca	aag	agg	att	aga	cag	taa	gag	ttt	624
Gly	Phe	Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln		Glu	Phe	
			185					190						195		
aca	aga	aat	aaa	tct	ata	ttt	ttg	tga	agg	gta	gtg	gta	tta	tac	tgt	672
Thr	Arg	Asn	Lys	Ser	Ile	Phe	Leu		Arg	Val	Val	Val	Leu	Tyr	Cys	
			200					205						210		
aga	ttt	cag	tag	ttt	cta	agt	ctg	tta	ttg	ttt	tgt	taa	caa	tgg	cag	720
Arg	Phe	Gln		Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys		Gln	Trp	Gln	

215	220	225	
gtt tta cac gtc tat gca att gta caa aaa agt tat aag aaa act aca	768		
Val Leu His Val Tyr Ala Ile Val Gln Lys Ser Tyr Lys Lys Thr Thr			
230	235	240	
tgt aaa atc ttg ata gct aaa taa ctt gcc att tct tta tat gga acg	816		
Cys Lys Ile Leu Ile Ala Lys Leu Ala Ile Ser Leu Tyr Gly Thr			
245	250	255	
cat ttt ggg ttg ttt aaa aat tta taa cag tta taa aga aag aat tat	864		
His Phe Gly Leu Phe Lys Asn Leu Gln Leu Arg Lys Asn Tyr			
260	265	270	
aaa gga aaa aga aaa taa cgc aat gga caa gtg gtg aag ctg tga act	912		
Lys Gly Lys Arg Lys Arg Asn Gly Gln Val Val Lys Leu Thr			
275	280		
cag gtg tgc aca att atc agg aac acc cca aaa cca aag tga ggt aga	960		
Gln Val Cys Thr Ile Ile Arg Asn Thr Pro Lys Pro Lys Gly Arg			
285	290	295	
aat agc atg aga agc cgt gtt tga tgt taa tta att	996		
Asn Ser Met Arg Ser Arg Val Cys Leu Ile			
300	305		

<210> 52  
 <211> 47  
 <212> PRT  
 <213> human

<400> 52

Phe Pro Ile Gln Cys Ile Val His Gln Arg Ser Ile Gln Glu Phe		
1	5	10
Ile Ile Ile Ile Phe Asn Pro Ser Lys Ser Arg Glu Lys Ile Ala		
	20	25
Thr Ser Thr Ile Ala Ser Glu Ala Ser Gln Gln Pro Glu Thr Ala		
	35	40
		45

Leu Lys

<210> 53  
 <211> 32  
 <212> PRT  
 <213> human

<400> 53

Lys Val Gly Val Ala Val Met Val Ala Val Ile Met Val Thr Asp		
1	5	10
Gly Trp Val Leu Val Met Val Val Val Val Val Lys Val Val Met		
		15



Val Val

<210> 54  
 <211> 1044  
 <212> DNA  
 <213> mouse

<400> 54

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ttcacaggct taagcagcca gtaaattgaca atttatgtgg tagtcaggct 50
actgtgctgg taatgggtgat cttagcaggc agagaagggtg gtagtgattt 100
gatagtaaaa gtgtagacta tacaacagaa taaatacaag tatagtaaat 150
ccaacaaagt gtgaaagggtg tgtgccatta cacatctttc tcggtgataa 200
gagccttgct tatgaagttc tgagatgtgt taggaagatg aatcatcaat 250
ttacatttct ccccatcaaa tgacaccatg ctgatccagt attaagctaa 300
tactaacacc atgcaatgct tcattaacaa ggatttgctt cttgctagaa 350
atgggtaaaa acggactgtg gtctgtatac cttcaatgca gcttatgtgt 400
tgtcttttcc tgaaatggta atgactccca atagtggcaa ccaggggtac 450
aatacttgca cactttgtaa actctttctt tctctttggt ttccaggaca 500
caatgtagga agccttttcc acatggcaga tgatttgggc agagcgatgg 550
agtccttagt ttcagtcatg acagatgaag aaggagcaga ataaatgttt 600
tacaactcct gattcccgca tggtttttat aatattcgta caacaaagag 650
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tatggaacgc attttgggtt gtttaaaaaa ttataacagt tataaagaaa 900
gattgtaaac taaagtgtgc tttataaaaa agtttggtta taaaaacccc 950
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ctgaggcagc acattgtttt gcattacttt agcgtgtatc atat 1044

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<210> 55  
 <211> 1236

<212> DNA  
<213> human

<400> 55

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ttattattat tttcaacca agtaaaagca gagagaaaat agccacctcc 100
accatagcct cagaagcaag ccaacagcct gaaacagctt tgaaatgaaa 150
agttggtgtg gcggtgatgg tggcagtgat aatggtgacc gatggttggg 200
tgctggtgat ggtagtggta gttgtga.ag gtggtgatgg tggtttgatt 250
gatagtaaaa aaaatgttcg ttaatacaag tagagagtaa gtaatcaatc 300
aatcactcat agccaaggtg gaaaagatgt atcccatcat ggaatattcc 350
tgttctgata gaaatcttgt gcttatctat ggaattcttt tgatatatat 400
ttacattggg aacctgaatg tagcttgaca tttttccatg taaacaccag 450
tagcctgata caacattaag ctgatactaa caaacaacgt gtaatggctt 500
cattaataag gctttgcttc ttcctggaaa ctggtgaaaa atcaaacctt 550
gttgtgtaca ccctcgatgc agcttctgtg ttgtcttcac ccagaaatgg 600
ggaatgattt cccaatggc aaagaaacag agtgatgcta tctatctgca 650
ccttttgtaa agtctgtctt tctttctctt tgttttccag gacacaatgt 700
aggaagtctt ttccacatgg cagatgattt gggcagagcg atggagtcct 750
tagtatcagt catgacagat gaagaaggag cagaataaat gttttacaac 800
tcctgattcc cgcattggtt ttataatatt catacaacaa agaggattag 850
acagtaagag tttacaagaa at.aaatcta tatttttgtg aagggtagtg 900
gtattatact gtagatttca gtagtttcta agtctgttat tgttttgtta 950
acaatggcag gttttacacg tctatgcaat tgtacaaaaa agttataaga 1000
aaactacatg taaaatcttg atagctaaat aacttgccat ttctttatat 1050
ggaacgcatt ttgggttgtt taaaaattta taacagttat aaagaaagaa 1100
ttataaagga aaaagaaaat aacgcaatgg acaagtgggtg aagctgtgaa 1150
ctcaggtgtg cacaattatc aggaacaccc caaaaccaa gtgaggtaga 1200
aatagcatga gaagccgtgt ttgatgttaa ttaatt 1236
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<210> 56  
<211> 303

<212> PRT  
<213> human

<400> 56

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Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30
Asn	Val	Ala	Arg	His	Phe	Ser	Met	Lys	Thr	Pro	Val	Ala	Arg	Ser
				35					40					45
Asn	Ile	Lys	Leu	Ile	Leu	Thr	Asn	Asn	Val	Lys	Trp	Leu	His	Lys
				50					55					60
Lys	Gly	Phe	Ala	Ser	Ser	Trp	Lys	Leu	Val	Lys	Asn	Gln	Thr	Leu
				65					70					75
Leu	Cys	Thr	Pro	Ser	Met	Gln	Leu	Leu	Cys	Cys	Leu	His	Pro	Glu
				80					85					90
Met	Gly	Asn	Asp	Phe	Pro	Asn	Gly	Lys	Glu	Thr	Glu	Arg	Cys	Tyr
				95					100					105
Leu	Ser	Ala	Pro	Phe	Val	Lys	Ser	Val	Phe	Leu	Ser	Leu	Cys	Phe
				110					115					120
Pro	Gly	His	Asn	Val	Gly	Ser	Leu	Phe	His	Met	Ala	Asp	Asp	Leu
				125					130					135
Gly	Arg	Ala	Met	Glu	Ser	Leu	Val	Ser	Val	Met	Thr	Asp	Glu	Glu
				140					145					150
Gly	Ala	Glu	Lys	Met	Phe	Tyr	Asn	Ser	Arg	Phe	Pro	His	Gly	Phe
				155					160					165
Tyr	Asn	Ile	His	Thr	Thr	Lys	Arg	Ile	Arg	Gln	Lys	Glu	Phe	Thr
				170					175					180
Arg	Asn	Lys	Ser	Ile	Phe	Leu	Arg	Arg	Val	Val	Val	Leu	Tyr	Cys
				185					190					195
Arg	Phe	Gln	Lys	Phe	Leu	Ser	Leu	Leu	Leu	Phe	Cys	Lys	Gln	Trp
				200					205					210
Gln	Val	Leu	His	Val	Tyr	Ala	Ile	Val	Gln	Lys	Ser	Tyr	Lys	Lys
				215					220					225
Thr	Thr	Cys	Lys	Ile	Leu	Ile	Ala	Lys	Lys	Leu	Ala	Ile	Ser	Leu
				230					235					240
Tyr	Gly	Thr	His	Phe	Gly	Leu	Phe	Lys	Asn	Leu	Lys	Gln	Leu	Lys
				245					250					255
Arg	Lys	Asn	Tyr	Lys	Gly	Lys	Arg	Lys	Lys	Arg	Asn	Gly	Gln	Val

	260		265		270									
Val	Lys	Leu	Arg	Thr	Gln	Val	Cys	Thr	Ile	Ile	Arg	Asn	Thr	Pro
				275					280					285
Lys	Pro	Lys	Arg	Gly	arg	Asn	Ser	Met	Arg	Ser	Arg	Val	Arg	Cys
				290					295					300

Lys Leu Ile

<210> 57  
 <211> 111  
 <212> DNA  
 <213> human

<400> 57  
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 aaaagttggtt tataaaaacc cctaaaaaca aaacaaacac acacacacac 100  
 acatacacac a 111

<210> 58  
 <211> 260  
 <212> DNA  
 <213> human

<400> 58  
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 AACATCAAAC ACGGCTTCTC ATGCTATTTT TACCTCACTT TGGTTTTGGG 100  
 GTGTTCTCTGA TAATTGTGCA CACCTGAGTT CACAGCTTCA CCACTTGTCC 150  
 ATTGCGTTAT TTTCTTTTTC CTTTATAATT CTTTCTTTTT CCTTCATAAT 200  
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 ACAAGTGGTG 260

<210> 59  
 <211> 17  
 <212> DNA  
 <213> human

<400> 59

gccctcattc tggagac

17

<210> 60  
 <211> 17  
 <212> DNA

<213> human

<400> 60

gcggtgatgg tggcagt

17

<210> 61

<211> 107

<212> PRT

<213> human

<400> 61

Met	Tyr	Pro	Ile	Met	Glu	Tyr	Ser	Cys	Ser	Asp	Arg	Asn	Leu	Val
1				5					10					15

Leu	Ile	Tyr	Gly	Ile	Leu	Leu	Ile	Tyr	Ile	Tyr	Ile	Gly	Asn	Leu
				20					25					30

Asn	Met	Lys	Lys	Glu	Gln	Asn	Lys	Cys	Phe	Thr	Thr	Pro	Asp	Ser
				35					40					45

Arg	Met	Val	Phe	Ile	Ile	Phe	Ile	Gln	Gln	Arg	Gly	Leu	Asp	Ser
				50					55					60

Lys	Ser	Leu	Gln	Glu	Ile	Asn	Leu	Tyr	Phe	Cys	Glu	Gly	Phe	Tyr
				65					70					75

Thr	Ser	Met	Gln	Leu	Tyr	Lys	Lys	Val	Ile	Arg	Lys	Leu	His	Lys
				80					85					90

Ile	Thr	Gln	Trp	Thr	Arg	Thr	Pro	Gln	Asn	Gln	Ser	Glu	Val	Glu
				95					100					105

Ile Ala